

SEQUENCE LISTING

<110> C. Frank Bennett
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION

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acttctgaga aggttgcgca cagctgtgcc cggcagtcta gaggcgcaga agaggaagcc 180

atcgctggc cccggctctc tggaccttgt ctgctcggg agcggaaca gcggcagcca 240

gagaactgtt ttaatc atg gac aaa caa aac tca cag atg aat gct tct cac 292

Met Asp Lys Gln Asn Ser Gln Met Asn Ala Ser His

1

5

10

ccg gaa aca aac ttg cca gtt ggg tat cct cct cag tat cca ccg aca 340

Pro Glu Thr Asn Leu Pro Val Gly Tyr Pro Pro Gln Tyr Pro Pro Thr

15

20

25

gca ttc caa gga cct cca gga tat agt ggc tac cct ggg ccc cag gtc 388

Ala Phe Gln Gly Pro Pro Gly Tyr Ser Gly Tyr Pro Gly Pro Gln Val

30

35

40

agc tac cca ccc cca cca gcc ggc cat tca ggt cct ggc cca gct ggc 436

Ser Tyr Pro Pro Pro Pro Ala Gly His Ser Gly Pro Gly Pro Ala Gly

45

50

55

60

ttt cct gtc cca aat cag cca gtg tat aat cag cca gta tat aat cag 484

Phe Pro Val Pro Asn Gln Pro Val Tyr Asn Gln Pro Val Tyr Asn Gln

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70

75

cca gtt gga gct gca ggg gta cca tgg atg cca gcg cca cag cct cca 532

Pro Val Gly Ala Ala Gly Val Pro Trp Met Pro Ala Pro Gln Pro Pro

80

85

90

tta aac tgt cca cct gga tta gaa tat tta agt cag ata gat cag ata 580

Leu Asn Cys Pro Pro Gly Leu Glu Tyr Leu Ser Gln Ile Asp Gln Ile

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ctg att cat cag caa att gaa ctt ctg gaa gtt tta aca ggt ttt gaa			628
Leu Ile His Gln Gln Ile Glu Leu Leu Glu Val Leu Thr Gly Phe Glu			
110	115	120	
act aat aac aaa tat gaa att aag aac agc ttt gga cag agg gtt tac			676
Thr Asn Asn Lys Tyr Glu Ile Lys Asn Ser Phe Gly Gln Arg Val Tyr			
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ttt gca gcg gaa gat act gat tgc tgt acc cga aat tgc tgt ggg cca			724
Phe Ala Ala Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Gly Pro			
	145	150	155
tct aga cct ttt acc ttg agg att att gat aat atg ggt caa gaa gtc			772
Ser Arg Pro Phe Thr Leu Arg Ile Ile Asp Asn Met Gly Gln Glu Val			
	160	165	170
ata act ctg gag aga cca cta aga tgt agc agc tgt tgt tgt ccc tgc			820
Ile Thr Leu Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Cys Pro Cys			
	175	180	185
tgc ctt cag gag ata gaa atc caa gct cct cct ggt gta cca ata ggt			868
Cys Leu Gln Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly			
	190	195	200
tat gtt att cag act tgg cac cca tgt cta cca aag ttt aca att caa			916
Tyr Val Ile Gln Thr Trp His Pro Cys Leu Pro Lys Phe Thr Ile Gln			
205	210	215	220
aat gag aaa aga gag gat gta cta aaa ata agt ggt cca tgt gtt gtg			964
Asn Glu Lys Arg Glu Asp Val Leu Lys Ile Ser Gly Pro Cys Val Val			
	225	230	235
tgc agc tgt tgt gga gat gtt gat ttt gag att aaa tct ctt gat gaa			1012
Cys Ser Cys Cys Gly Asp Val Asp Phe Glu Ile Lys Ser Leu Asp Glu			
	240	245	250
cag tgt gtg gtt ggc aaa att tcc aag cac tgg act gga att ttg aga			1060
Gln Cys Val Val Gly Lys Ile Ser Lys His Trp Thr Gly Ile Leu Arg			
	255	260	265
gag gca ttt aca gac gct gat aac ttt gga atc cag ttc cct tta gac			1108
Glu Ala Phe Thr Asp Ala Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp			

270 275 280

ctt gat gtt aaa atg aaa gct gta atg att ggt gcc tgt ttc ctc att 1156
Leu Asp Val Lys Met Lys Ala Val Met Ile Gly Ala Cys Phe Leu Ile
285 290 295 300

gac ttc atg ttt ttt gaa agc act ggc agc cag gaa caa aaa tca gga 1204
Asp Phe Met Phe Phe Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly
305 310 315

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Val Trp

gactatctaa actcacact gtatgaatta agctgtaagg cctgtagctc tggttgtata 1323

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ctccttcact ctaaaactct ggtattataa cttttgaaag ttaatatttc tacatgaaat 1923

gtttagctct tacactctat ccttcctaga aaatggtaat tgagattact cagatattaa 1983

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agtcgctgct ggtgctagga ttctaggaat tcgcctcact tggagctgca tgagaaaaga	180
aaggcttgca a atg gag gct cct cgc tca gga aca tac ttg cca gct ggg	230
Met Glu Ala Pro Arg Ser Gly Thr Tyr Leu Pro Ala Gly	
1 5 10	
tat gcc cct cag tat cct cca gca gca gtc caa gga cct cca gag cat	278
Tyr Ala Pro Gln Tyr Pro Pro Ala Ala Val Gln Gly Pro Pro Glu His	
15 20 25	
act gga cgc ccc aca ttc cag act aac tac caa gtt ccc cag tct ggt	326
Thr Gly Arg Pro Thr Phe Gln Thr Asn Tyr Gln Val Pro Gln Ser Gly	
30 35 40 45	
tat cca gga cct cag gct agc tac aca gtc tca aca tct gga cat gaa	374
Tyr Pro Gly Pro Gln Ala Ser Tyr Thr Val Ser Thr Ser Gly His Glu	
50 55 60	
ggg tat gct gct aca cgg ctt cct att caa aat aat cag act ata gtc	422
Gly Tyr Ala Ala Thr Arg Leu Pro Ile Gln Asn Asn Gln Thr Ile Val	
65 70 75	
ctt gca aac act cag tgg atg cca gca cca cca cct att ctg aac tgc	470
Leu Ala Asn Thr Gln Trp Met Pro Ala Pro Pro Pro Ile Leu Asn Cys	
80 85 90	
cca cct ggg cta gaa tac tta aat cag ata gat cag ctt ctg att cat	518
Pro Pro Gly Leu Glu Tyr Leu Asn Gln Ile Asp Gln Leu Leu Ile His	
95 100 105	
cag caa gtt gaa ctt cta gaa gtc tta aca ggc ttt gaa aca aat aac	566
Gln Gln Val Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn	
110 115 120 125	
aaa ttt gaa atc aag aac agc ctc ggg cag atg gtt tat gtt gca gtg	614
Lys Phe Glu Ile Lys Asn Ser Leu Gly Gln Met Val Tyr Val Ala Val	
130 135 140	
gaa gat act gac tgc tgt act cga aat tgc tgt gaa gcg tct aga cct	662

Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Glu Ala Ser Arg Pro	
145 150 155	
ttc acc tta aga atc ctg gat cat ctg ggc caa gaa gtc atg act ctg	710
Phe Thr Leu Arg Ile Leu Asp His Leu Gly Gln Glu Val Met Thr Leu	
160 165 170	
gag cga cct ctg aga tgc agt agc tgc tgc ttc ccc tgc tgc ctc cag	758
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175 180 185	
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Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Thr	
190 195 200 205	
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Arg Glu Asn Val Leu Lys Val Val Gly Pro Cys Val Ala Cys Thr Cys	
225 230 235	
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Cys Ser Asp Ile Asp Phe Glu Ile Lys Ser Leu Asp Glu Val Thr Arg	
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Ile Gly Lys Ile Thr Lys Gln Trp Ser Gly Cys Val Lys Glu Ala Phe	
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Thr Asp Ser Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Glu Val	
270 275 280 285	
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Lys Met Lys Ala Val Thr Leu Gly Ala Cys Phe Leu Ile Asp Tyr Met	
290 295 300	
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Phe Phe Glu Gly Cys Glu	
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27

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ttaaactgtc cacctggatt agaatattta agtcaggtaa tttcaaagac acaaaatact 180

cataaaaaac agaactgtgc ttccagcttg cttaaccaga ttagcaaagc aataattcac 240

caaagtctga aatagcaaaa ctgtatttcc tgctaacaga ttactctaatt tttcttaggt 300

ctgggttcaat tttaaagcaa aatacaaatg ccttagaaaa ttgtattttc tggtatctta 360

aatacaatct atgataatgg ccaatagcaa acatttaatt agcactgttt cctgcctttg 420

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caaatttgaa agtacttttg ctataagttt cctaaaagta ttttaatactt ttttttttca 360
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gacttcatgt tttttgaaag ccctggcagc caggaacaaa aatcaggagt gtggtagtgg 180
attagtgaaa gtctcctcag gaaatctgaa gtctgtatat tgattgagac tatctaaact 240
catacctgta tgaattaagc tgtaaggcct gtagctctgg ttgtatactt ttgcttttca 300
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